

21374583.txt
SEQUENCE LISTING

<110> Bander, Neil H.

<120> TREATMENT AND DIAGNOSIS OF CANCER

<130> Lois M. Kwasigroch: BZL 242/028

<140> US 09/357,708

<141> 1999-07-20

<150> US 08/895,914

<151> 1997-07-17

<150> US 08/838,682

<151> 1997-04-09

<150> US 60/016,976

<151> 1996-05-06

<150> US 60/022,125

<151> 1996-07-18

<160> 21

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> MUS sp.

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tgaatataacc atacaactggg tgaagcagag ccatggaaag agccttgagt ggattggaaa 180
catcaatcct aacaatggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt 240
gactgttagac aagtccctcca gtacagccta catggagctc cgccgcctaa catctgagga 300
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gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt 180
gtagggtggta ccaccattgt taggattgtat gtttccaatc cactcaaggc tctttccatg 240
gcctctgcttc acccagtgtt ggttatattc agtgaatgtg tatccagaag tcttgcagga 300
tatcctcact gaagtcccag gcttcaccag ttccaggccca gactgttgcgacttgc 360
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<210> 3

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<400> 3

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					20		25					30			
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro
							40				45				

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Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
50 55 60

Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
65 70 75 80

Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
85 90 95

Ser Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His
100 105 110

His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
115 120

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<213> Mus sp.

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Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
35 40 45

Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
50 55 60

Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
65 70 75 80

Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
85 90 95

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
115 120 125

Thr Pro
130

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 20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
 35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
 50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
 65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
 85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
 100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
 115 120 125

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 aatcagaagt tcgaggacaa ggccacattg actgttagaca agtcctccag tacagcctac 240
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attgttagga	ttgatgttcc	caatccactc	aaggctctt	ccatggctct	gcttcaccca	240
gtgtatggta	tattcagtga	atgtgtatcc	agaagtcttg	caggatatcc	tcactgaagt	300
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20					25					30					

Thr	Ile	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile
35					40					45					

Gly	Asn	Ile	Asn	Pro	Asn	Asn	Gly	Gly	Thr	Thr	Tyr	Asn	Gln	Lys	Phe
50					55				60						

Glu	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
65				70				75					80		

Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
	85					90						95			

Ala	Ala	Gly	Trp	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr
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	115														

<210> 9

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<212> DNA

<213> Mus sp.

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gtaggagaga	gggtcacctt	gacctgcaag	gccagtgaga	atgtggttac	ttatgtttcc										120

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tacactgggg tccccgatcg cttcacaggc	agtggatctg caacagattt cactctgacc	240
atcagcagtg tgccaggctga agaccttgca	gattatcaact gtggacaggg ttacagctat	300
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gta		363

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gtaccggttg gatccccgt atatcagcag ttttaggagac	tgctctggtt tctgttata	240
ccagggaaaca taagtaacca cattctcaact ggccttgcag	gtcaaggta ccctctctcc	300
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taa		363

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20 25 30	

Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln	
35 40 45	

Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val	
50 55 60	

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr	
Page 6	

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65 70 75 80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
85 90 95
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110
Lys Arg Ala Asp Ala Ala Pro Thr Val
115 120

<210> 12
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<213> Mus sp.

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Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60
Ala Val Asp Leu Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gln Leu Met Leu His Gln
100 105 110
Leu Tyr

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<212> PRT
<213> Mus sp.

<400> 13
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Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
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Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
40 45
Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
55
Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
70 75 80
Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
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Cys Thr Asn Cys
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cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
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<210> 15

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caoccagttta ggagactgct ctggtttctg ttgataccag gaaacataag taaccacatt 240

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Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile	
35	40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
50	55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala	
65	70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr	
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Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	
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<210> 17

<211> 321

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ggacaatctc ctaaaactact gatttattgg gcattccactc ggcacacgtgg agtccctgtat	180
cgcttcacag gcagtggatc tgggacagac ttcaactctca ccattactaa tgttcagtct	240
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gggaccatgc tggacctgaa a	321

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<211> 321

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agatccactg	c当地	gatcaggac	tccagtgtgc	cgagtggatg	cccaataaat	180
cagtagttt	ggagattgtc	ctggtttctg	ttgataccag	tctacagcag	taccacatc	240
ttgactggcc	ttacagatga	tgctgaccct	gtctctact	gatgtggaca	tgaatttgtg	300
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Asp	Arg	Val	Ser	Ile	Ile	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Thr	Ala
	20						25					30			

Val	Asp	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
	35			40					45						

Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
50					55				60						

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Asn	Val	Gln	Ser
65				70				75					80		

Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Leu
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Thr	Phe	Gly	Ala	Gly	Thr	Met	Leu	Asp	Leu	Lys					
	100					105									

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21374583.txt

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20 25 30

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35 40 45

Ile Gly Asp Ile Asn Pro Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Tyr Tyr Ser Ser Ser Tyr Met Ala Tyr Tyr Ala Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 21

<211> 109

<212> PRT

<213> Mus sp.

<400> 21

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Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
65 70 75 80

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
85 90 95

Pro Arg Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105